



SEQUENCE LISTING

#10
RECEIVED
JUN 26 2002
TECH CENTER 1600/2900

<110> Fouser, Lynette
Liu, Wei
Deng, Bijia

<120> TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING
SAME

<130> 22058-532

<140> 10/047264

<141> 2002-01-14

<150> 60/261442

<151> 2001-01-12

<150> 60/267021

<151> 2001-02-06

<150> 60/270835

<151> 2001-02-23

<160> 39

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Human

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Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly		
65	70	75
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln		
85	90	95
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser		
100	105	110
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile		
115	120	125
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val		
130	135	140
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn		
145	150	155
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile		
165	170	175
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg		
180	185	190
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val		
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Arg	Val	Gln	Phe	Gln	Ser	Arg	Asn	Phe	His	Asn	Ile	Leu	Gln	Trp	Gln
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Pro	Gly	Arg	Ala	Leu	Thr	Gly	Asn	Ser	Ser	Val	Tyr	Phe	Val	Gln	Tyr
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Lys	Ile	Met	Phe	Ser	Cys	Ser	Met	Lys	Ser	Ser	His	Gln	Lys	Pro	Ser
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Gly	Cys	Trp	Gln	His	Ile	Ser	Cys	Asn	Phe	Pro	Gly	Cys	Arg	Thr	Leu
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Ala	Lys	Tyr	Gly	Gln	Arg	Gln	Trp	Lys	Asn	Lys	Glu	Asp	Cys	Trp	Gly
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Ile	Leu	His	Ala	Pro	Asn	Leu	Pro	Tyr	Arg	Tyr	Gln	Lys	Glu	Lys	Asn
		180						185					190		
Val	Ser	Ile	Glu	Asp	Tyr	Tyr	Glu	Leu	Leu	Tyr	Arg	Val	Phe	Ile	Ile
		195					200					205			
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	210					215					220				
Ala	Val	Glu	Ile	Glu	Ala	Leu	Thr	Pro	His	Ser	Ser	Tyr	Cys	Val	Val
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35 40 45
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95
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Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Arg Ala Lys
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<210> 7
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

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 35 40 45
 Asn Leu Ser Tyr Thr Val Gln Ala Lys Ser Ile Phe Pro Lys Gln Asn
 50 55 60
 Phe Asn Asn Val Thr Thr Asn Leu Asn Val Thr Glu Cys Asp Val Ser
 65 70 75 80
 Ser Leu Ser Val Tyr Gly Ala Tyr Val Leu Arg Val Arg Thr Glu Trp
 85 90 95
 Glu Asp Glu His Ser Asp Trp Ala Val Val Arg Phe Lys Pro Met Ala
 100 105 110
 Asp Thr Val Ile Gly Pro Pro Ser Val Asn Val Lys Ser Glu Ser Gly
 115 120 125
 Thr Leu His Val Asp Phe Thr Gly Pro Ala Ala Asp Arg Glu His Asp
 130 135 140
 Lys Trp Ser Leu Lys Gln Tyr Tyr Gly Ser Trp Ile Tyr Arg Ile Leu
 145 150 155 160
 Tyr Trp Lys Lys Gly Ser Asn Lys Lys Val Ile His Ile Asp Thr Lys
 165 170 175
 His Asn Ser Glu Ile Leu Ser Gln Leu Glu Pro Trp Thr Ile Tyr Cys
 180 185 190
 Ile Gln Val Gln Gly Val Ile Pro Glu Trp Asn Lys Thr Gly Glu Arg
 195 200 205

Ser Gln Glu Leu Cys Glu Gln Thr Thr His Asn Gly Val Thr Pro Val
 210 215 220
 Trp Ile Val Val Thr Val Leu Leu Gly Ser Met Leu Ala Val Ile Ile
 225 230 235 240
 Ser Val Pro Val Cys Phe Phe Ala Phe Trp Tyr Leu Tyr Arg Phe Thr
 245 250 255
 Lys His Val Phe Phe Pro Ser Tyr Ile Phe Pro Gln His Leu Lys Glu
 260 265 270
 Phe Phe Ser Pro Val Pro Gln Glu Glu His His Phe His Asp Trp Leu
 275 280 285
 Thr Val Ile Ser Glu Glu Pro Lys Ser Gln Arg Asp Glu Thr Val Glu
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 Glu Ala Ser Arg Thr Ala Glu His His Gln Asp Ser Lys Gln Glu Ile
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<220>
 <223> Description of Artificial Sequence: PCR Primer

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<210> 10
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 <213> Artificial Sequence

<220>
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ctcagagagc tgttgaaatt gaaggtctga tacctcattc cagctactgc gtagtggtg 660
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<212> PRT
<213> human

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35 40 45
Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys
50 55 60
Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr
65 70 75 80
Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu
85 90 95
Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala
100 105 110
Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp
115 120 125
Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu
130 135 140
Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala
145 150 155 160
Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn
165 170 175
Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala
180 185 190

Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala
 195 200 205

Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys Glu
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Arg Cys Val Gln Ile Pro
 225 230

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<223> Wherein X is the amino acid I or V

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<221> VARIANT
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<223> Wherein X is the amino acid M or I

<220>
<221> VARIANT
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<210> 16
<211> 16
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<213> human

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<210> 17
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<220>
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<220>
<221> VARIANT
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Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

Glu Arg Cys Val Glu Ile Pro
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<210> 21
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Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
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35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

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<212> PRT

<213> human

<400> 22

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 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205
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 Glu Arg Cys Val Glu Ile Pro
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 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 24
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 <212> PRT
 <213> human

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 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu His Pro Gln
 20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly

65		70		75		80									
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				85					90					95	
Glu	Pro	Tyr	Tyr	Gly	Arg	Val	Arg	Ala	Ala	Ser	Ala	Gly	Ser	Tyr	Ser
			100					105					110		
Glu	Trp	Ser	Met	Thr	Pro	Arg	Phe	Thr	Pro	Trp	Trp	Glu	Thr	Lys	Ile
		115					120					125			
Asp	Pro	Pro	Val	Met	Asn	Ile	Thr	Gln	Val	Asn	Gly	Ser	Leu	Leu	Val
	130					135					140				
Ile	Leu	His	Ala	Pro	Asn	Leu	Pro	Tyr	Arg	Tyr	Gln	Lys	Glu	Lys	Asn
145					150					155					160
Val	Ser	Ile	Glu	Asp	Tyr	Tyr	Glu	Leu	Leu	Tyr	Arg	Val	Phe	Ile	Ile
			165					170						175	
Asn	Asn	Ser	Leu	Glu	Lys	Glu	Gln	Lys	Val	Tyr	Glu	Gly	Ala	His	Arg
		180						185					190		
Ala	Val	Glu	Ile	Glu	Ala	Leu	Thr	Pro	His	Ser	Ser	Tyr	Cys	Val	Val
		195					200					205			
Ala	Glu	Ile	Tyr	Gln	Pro	Met	Leu	Asp	Arg	Arg	Ser	Gln	Arg	Ser	Glu
	210					215					220				
Glu	Arg	Cys	Val	Glu	Ile	Pro									
225					230										
<210> 25															
<211> 231															
<212> PRT															
<213> human															
<400> 25															
Met	Met	Pro	Lys	His	Cys	Phe	Leu	Gly	Phe	Leu	Ile	Ser	Phe	Phe	Leu
1				5					10					15	
Thr	Gly	Val	Ala	Gly	Thr	Gln	Ser	Thr	His	Glu	Ser	Leu	Lys	Pro	Gln
		20						25					30		
Lys	Val	Gln	Phe	Gln	Ser	Arg	Asn	Phe	His	Asn	Ile	Leu	Gln	Trp	Gln
		35					40					45			
Pro	Gly	Arg	Ala	Leu	Thr	Gly	Asn	Ser	Ser	Val	Tyr	Phe	Val	Gln	Tyr
	50					55					60				
Lys	Ile	Tyr	Gly	Gln	Arg	Gln	Trp	Lys	Asn	Lys	Glu	Asp	Cys	Trp	Gly
65					70					75					80
Thr	Gln	Glu	Leu	Ser	Cys	Asp	Leu	Thr	Ser	Glu	Thr	Ser	Asp	Ile	Gln
				85					90					95	

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 26
 <211> 231
 <212> PRT
 <213> human

<400> 26

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30

Arg Val Gln Phe Gln Ser Arg Gln Phe His Asn Ile Leu Gln Trp Gln
 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 27
 <211> 231
 <212> PRT
 <213> human

<400> 27
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Val Gln Trp Gln
 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn

145		150		155		160
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	165	170	175			
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	180	185	190			
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	195	200	205			
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu	210	215	220			
Glu Arg Cys Val Glu Ile Pro	225	230				
<210> 28						
<211> 231						
<212> PRT						
<213> human						
<400> 28						
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu	1	5	10	15		
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln	20	25	30			
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	35	40	45			
Pro Gly Arg Leu Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	50	55	60			
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	65	70	75	80		
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	85	90	95			
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	100	105	110			
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	115	120	125			
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	130	135	140			
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	145	150	155	160		
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	165	170	175			

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

<210> 29

<211> 231

<212> PRT

<213> human

<400> 29

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Ala Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 30
 <211> 231
 <212> PRT
 <213> human

<400> 30
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Ile Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

Glu Arg Cys Val Glu Ile Pro

225

230

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 31
gaattcgtcg acccaccatg cctaagcatt gccttc 36

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 32
tggaatctgc acacatctct cc 22

<210> 33
<211> 199
<212> PRT
<213> human

<220>
<221> VARIANT
<222> (139)
<223> Wherein "X" is a space inserted in the Blast
alignment analysis.

<400> 33
Lys Pro Gln Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu
1 5 10 15
Gln Trp Gln Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe
20 25 30
Val Gln Tyr Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp
35 40 45
Cys Trp Gly Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser
50 55 60
Asp Ile Gln Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly
65 70 75 80
Ser Tyr Ser Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu
85 90 95

Thr Lys Ile Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser
 100 105 110
 Leu Leu Val Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys
 115 120 125
 Glu Lys Asn Val Ser Ile Glu Asp Tyr Tyr Xaa Glu Leu Leu Tyr Arg
 130 135 140
 Val Phe Ile Ile Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu
 145 150 155 160
 Gly Ala His Arg Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser
 165 170 175
 Tyr Cys Val Val Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser
 180 185 190
 Gln Arg Ser Glu Glu Arg Cys
 195

<210> 34
 <211> 231
 <212> PRT
 <213> human

<400> 34
 Ser Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu Leu
 1 5 10 15
 Ser Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Pro Gln
 20 25 30
 Lys Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln
 35 40 45
 Ala Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr
 50 55 60
 Lys Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly
 65 70 75 80
 Thr Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr
 85 90 95
 Glu Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser
 100 105 110
 Ala Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu
 115 120 125
 Asp Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val
 130 135 140
 Leu Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn
 145 150 155 160

Ala Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg
180 185 190

Ala Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys
210 215 220

Glu Arg Cys Val Gln Ile Pro
225 230

<210> 35

<211> 231

<212> PRT

<213> human

<400> 35

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg

180	185	190
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val		
195	200	205
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu		
210	215	220
Glu Arg Cys Val Glu Ile Pro		
225	230	

<210> 36
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR Primer

<400> 36
 cttgcaacca tgatgcctaa acattgc 27

<210> 37
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR Primer

<400> 37
 atgatgccta aacattgctt tctagg 26

<210> 38
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR Primer

<400> 38
 ggaactctgg ttgccagaca agcacac 27

<210> 39
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR Primer

<400> 39

caaggagaga tgtgtgcaga ttccatga

28